

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/069,228

DATE: 05/08/98  
TIME: 12:48:09

INPUT SET: S25681.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

(1) General Information:

(i) APPLICANT: Gregory Plowman  
Douglas Clary

(ii) TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF  
Alk-7 RELATED DISORDERS

(iii) NUMBER OF SEQUENCES: 15

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Lyon & Lyon  
(B) STREET: 633 West Fifth Street  
Suite 4700  
(C) CITY: Los Angeles  
(D) STATE: California  
(E) COUNTRY: U.S.A.  
(F) ZIP: 90071-2066

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
storage  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: IBM P.C. DOS 5.0  
(D) SOFTWARE: FastSEQ for Windows 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To be assigned  
(B) FILING DATE: Filed herewith  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/044,428

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--> OK

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PATENT APPLICATION US/09/069,228DATE: 05/08/98  
TIME: 12:48:10

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47 (B) FILING DATE: April 28, 1997  
48  
49  
50 (viii) ATTORNEY/AGENT INFORMATION:  
51  
52 (A) NAME: Warburg, Richard J.  
53 (B) REGISTRATION NUMBER: 32,327  
54 (C) REFERENCE/DOCKET NUMBER: 234/118  
55  
56

57 (ix) TELECOMMUNICATION INFORMATION:  
58  
59 (A) TELEPHONE: (213) 489-1600  
60 (B) TELEFAX: (213) 955-0440  
61 (C) TELEX: 67-3510  
62  
63  
64

65 (2) INFORMATION FOR SEQ ID NO: 1:  
66

67 (i) SEQUENCE CHARACTERISTICS:  
68  
69 (A) LENGTH: 1793 base pairs  
70 (B) TYPE: nucleic acid  
71 (C) STRANDEDNESS: single  
72 (D) TOPOLOGY: linear  
73

74 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
75

76	CGGCCACACT	GACTAGAGCC	AACCGCGCAC	TTCAAAAGGG	TGTCGGTGCC	GCGCTCCCCT	60
77	CCCGCGGCC	GGGAACTTCA	AAGCGGGCCG	TGCTGCCCG	GCTGCCCTCGC	TCTGCTCTGG	120
78	GGCCTCGCAG	CCCCGGCGCG	GCCGCTGGT	GGCGATGACC	CGGGCGCTCT	GCTCAGCGCT	180
79	CCGCCAGGCT	CTCCTGCTGC	TCGCAGCGGC	CGCCGAGCTC	TCGCCAGGAC	TGAAGTGTGT	240
80	ATGTCTTTTG	TGTGATTCTT	CAAACTTTAC	CTGCCAAACA	GAAGGAGCAT	GTTGGGCATC	300
81	AGTCATGCTA	ACCAATGGAA	AAGAGCAGGT	GATCAAAATCC	TGTGTCTCCC	TTCCAGAACT	360
82	GAATGCTCAA	GTCTTCTGTC	ATAGTTCCAA	CAATGTTACC	AAAACCGAAT	GCTGCTTCAC	420
83	AGATTTTTGC	AACAACATAA	CACTGCACCT	TCCAACAGCA	TCACCAAATG	CCCCAAAAC	480
84	TGGACCCATG	GAGCTGGCCA	TCATTATTAC	TGTGCCCTGTT	TGCCCTCCTGT	CCATAGCTGC	540
85	GATGCTGACA	GTATGGGCAT	GCCAGGGTCG	ACAGTGCTCC	TACAGGAAGA	AAAAGAGACC	600
86	AAATGTGGAG	GAACCACTCT	CTGAGTGCAA	TCTGGTAAAT	GCTGGAAAAA	CTCTGAAAGA	660
87	TCTGATTTAT	GATGTGACCG	CCTCTGGATC	TGGCTCTGGT	CTACCTCTGT	TGGTTCAAAG	720
88	GACAAATGCA	AGGACGATTG	TGCTTCAGGA	AATAGTAGGA	AAAGGTAGAT	TTGGTGAGGT	780
89	GTGGCATGGA	AGATGGTGTG	GGGAAGATGT	GGCTGTGAAA	ATATTCTCCT	CCAGAGATGA	840
90	AAGATCTTGG	TTTCGTGAGG	CAGAAATTTA	CCAGACGGTC	ATGCTGCGAC	ATGAAAACAT	900
91	CCTTGTTTTC	ATTGCTGCTG	ACAACAAAGA	TAATGGAAC	TGGACTCAAC	TTTGGCTGGT	960
92	ATCTGAATAT	CATGAACAGG	GCTCCTTATA	TGACTATTTG	AATAGAAATA	TAGTGACCGT	1020
93	GGCTGGAATG	ATCAAGCTGG	CGCTCTCAAT	TGCTAGTGGT	CTGGCACACC	TTCATATGGA	1080
94	GATTGTTGGT	ACACAAGGTA	AACCTGCTAT	TGCTCATCGA	GACATAAAAT	CAAAGAATAT	1140
95	CTTAGTGAAA	AAGTGTGAAA	CTTGTTGCCAT	AGCGGACTTA	GGGTTGGCTG	TGAAGCATGA	1200
96	TTCAAATACTG	AACACTATCG	ACATACCTCA	GAATCCTAAA	GTGGGAACCA	AGAGGTATAT	1260
97	GGCTCCTGAA	ATGCTTGATG	ATACAATGAA	TGTGAATATC	TTTGAGTCC	TCAAACGAGC	1320
98	TGACATCTAT	TCTGTTGGTC	TGGTTTACTG	GGAAATAGCC	CGGAGGTGTT	CAGTCGGAGG	1380
99	AATTGTTGAG	GAGTACCAAT	TGCCTTATTA	TGACATGGTG	CCTTCAGATC	CCTCGATAGA	1440

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100 GGAAATGAGA AAGGTTGTTT GTGACCAGAA GTTTCGACCA AGTATCCCAA ACCAGTGGCA 1500
101 AAGTTGTGAA GCACTCCGAG TCATGGGGAG AATAATGCGT GAGTGTTGGT ATGCCAACGG 1560
102 AGCGGCCCGC CTAAGTCTC TTCGTATTAA GAAGACTATA TCTCAACTTT GTGTCAAAGA 1620
103 AGACTGCAAA GCCTAATGAT GATAATTATG TTAAGAAAGAA ATCTCTCATA GCTTTCCTTT 1680
104 CCATTTTCCC CTTTATGTGA ATGTTTTTGC CATTTCCTTTT TTGTTCTACC TCAAAGATAA 1740
105 GACAGTACAG TATTTAAGTG CCCATAAGGC AGCATGAAAA GATAACTCTA AAG 1793

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106

107

108

109 (2) INFORMATION FOR SEQ ID NO: 2:

110

111 (i) SEQUENCE CHARACTERISTICS:

112

113 (A) LENGTH: 493 amino acids

114 (B) TYPE: amino acid

115 (C) STRANDEDNESS: single

116 (D) TOPOLOGY: linear

117

118 (ii) MOLECULE TYPE: Peptide

119

120 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

121

122 Met Thr Arg Ala Leu Cys Ser Ala Leu Arg Gln Ala Leu Leu Leu Leu

123 1 5 10 15

124

125 Ala Ala Ala Ala Glu Leu Ser Pro Gly Leu Lys Cys Val Cys Leu Leu

126 20 25 30

127

128

129 Cys Asp Ser Ser Asn Phe Thr Cys Gln Thr Glu Gly Ala Cys Trp Ala

130 35 40 45

131

132 Ser Val Met Leu Thr Asn Gly Lys Glu Gln Val Ile Lys Ser Cys Val

133 50 55 60

134

135 Ser Leu Pro Glu Leu Asn Ala Gln Val Phe Cys His Ser Ser Asn Asn

136 65 70 75 80

137

138 Val Thr Lys Thr Glu Cys Cys Phe Thr Asp Phe Cys Asn Asn Ile Thr

139 85 90 95

140

141 Leu His Leu Pro Thr Ala Ser Pro Asn Ala Pro Lys Leu Gly Pro Met

142 100 105 110

143

144 Glu Leu Ala Ile Ile Ile Thr Val Pro Val Cys Leu Leu Ser Ile Ala

145 115 120 125

146

147 Ala Met Leu Thr Val Trp Ala Cys Gln Gly Arg Gln Cys Ser Tyr Arg

148 130 135 140

149

150 Lys Lys Lys Arg Pro Asn Val Glu Glu Pro Leu Ser Glu Cys Asn Leu

151 145 150 155 160

152

862240 82269060

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153	Val	Asn	Ala	Gly	Lys	Thr	Leu	Lys	Asp	Leu	Ile	Tyr	Asp	Val	Thr	Ala
154					165					170						175
155																
156	Ser	Gly	Ser	Gly	Ser	Gly	Leu	Pro	Leu	Leu	Val	Gln	Arg	Thr	Ile	Ala
157				180					185						190	
158																
159	Arg	Thr	Ile	Val	Leu	Gln	Glu	Ile	Val	Gly	Lys	Gly	Arg	Phe	Gly	Glu
160			195					200						205		
161																
162	Val	Trp	His	Gly	Arg	Trp	Cys	Gly	Glu	Asp	Val	Ala	Val	Lys	Ile	Phe
163		210					215					220				
164																
165	Ser	Ser	Arg	Asp	Glu	Arg	Ser	Trp	Phe	Arg	Glu	Ala	Glu	Ile	Tyr	Gln
166	225					230					235					240
167																
168	Thr	Val	Met	Leu	Arg	His	Glu	Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ala	Asp
169					245					250					255	
170																
171	Asn	Lys	Asp	Asn	Gly	Thr	Trp	Thr	Gln	Leu	Trp	Leu	Val	Ser	Glu	Tyr
172				260					265					270		
173																
174	His	Glu	Gln	Gly	Ser	Leu	Tyr	Asp	Tyr	Leu	Asn	Arg	Asn	Ile	Val	Thr
175			275					280					285			
176																
177	Val	Ala	Gly	Met	Ile	Lys	Leu	Ala	Leu	Ser	Ile	Ala	Ser	Gly	Leu	Ala
178		290					295					300				
179																
180	His	Leu	His	Met	Glu	Ile	Val	Gly	Thr	Gln	Gly	Lys	Pro	Ala	Ile	Ala
181	305					310					315					320
182																
183	His	Arg	Asp	Ile	Lys	Ser	Lys	Asn	Ile	Leu	Val	Lys	Lys	Cys	Glu	Thr
184					325					330					335	
185																
186	Cys	Ala	Ile	Ala	Asp	Leu	Gly	Leu	Ala	Val	Lys	His	Asp	Ser	Ile	Leu
187				340					345					350		
188																
189	Asn	Thr	Ile	Asp	Ile	Pro	Gln	Asn	Pro	Lys	Val	Gly	Thr	Lys	Arg	Tyr
190			355					360					365			
191																
192																
193	Met	Ala	Pro	Glu	Met	Leu	Asp	Asp	Thr	Met	Asn	Val	Asn	Ile	Phe	Glu
194		370					375					380				
195																
196	Ser	Phe	Lys	Arg	Ala	Asp	Ile	Tyr	Ser	Val	Gly	Leu	Val	Tyr	Trp	Glu
197	385					390					395					400
198																
199	Ile	Ala	Arg	Arg	Cys	Ser	Val	Gly	Gly	Ile	Val	Glu	Glu	Tyr	Gln	Leu
200					405					410					415	
201																
202	Pro	Tyr	Tyr	Asp	Met	Val	Pro	Ser	Asp	Pro	Ser	Ile	Glu	Glu	Met	Arg
203				420					425					430		
204																
205	Lys	Val	Val	Cys	Asp	Gln	Lys	Phe	Arg	Pro	Ser	Ile	Pro	Asn	Gln	Trp

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206                   435                   440                   445  
207  
208   Gln Ser Cys Glu Ala Leu Arg Val Met Gly Arg Ile Met Arg Glu Cys  
209           450                   455                   460  
210  
211   Trp Tyr Ala Asn Gly Ala Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys  
212   465                   470                   475                   480  
213  
214   Thr Ile Ser Gln Leu Cys Val Lys Glu Asp Cys Lys Ala  
215                   485                   490  
216  
217  
218

## (2) INFORMATION FOR SEQ ID NO: 3:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:           8 amino acids  
(B) TYPE:             amino acid  
(C) STRANDEDNESS:    single  
(D) TOPOLOGY:        linear

(ii) MOLECULE TYPE:    Peptide

## (ix) FEATURE:

(D) OTHER INFORMATION:    "Xaa" in positions 6 and 7 stand  
                              for an unspecified amino acid.

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

His Arg Asp Leu Lys Xaa Xaa Asn  
1                   5

## (2) INFORMATION FOR SEQ ID NO: 4:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:           23 base pairs  
(B) TYPE:             nucleic acid  
(C) STRANDEDNESS:    single  
(D) TOPOLOGY:        linear

## (ix) FEATURE:

(D) OTHER INFORMATION:    The letter "R" stands for A or G.  
                              The letter "N" stands for Inosine.

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

PAGE: 1

**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/09/069,228**

DATE: 05/08/98  
TIME: 12:48:12

*INPUT SET: S25681.raw*

Line	Error	Original Text
39	Wrong application Serial Number	(A) APPLICATION NUMBER: To be assigned

09069060" 82269060